

0280

OIPE

#2

RAW SEQUENCE LISTING  
PATENT APPLICATION: US/10/003,392

DATE: 12/13/2001  
TIME: 09:12:54

Input Set : A:\BB1463 US NA Seq Listing.txt  
Output Set: N:\CRF3\12132001\I003392.raw

3 <110> APPLICANT: Allen, Stephen M.  
4 Caimi, Perry G.  
5 Stoop, Johan M.  
7 <120> TITLE OF INVENTION: Fructan Biosynthetic Enzymes  
9 <130> FILE REFERENCE: BB1463 US NA  
C--> 11 <140> CURRENT APPLICATION NUMBER: US/10/003,392  
C--> 12 <141> CURRENT FILING DATE: 2001-10-30  
14 <150> PRIOR APPLICATION NUMBER: 60/244,273  
15 <151> PRIOR FILING DATE: 2000-10-10  
17 <150> PRIOR APPLICATION NUMBER: 60/269,543  
18 <151> PRIOR FILING DATE: 2001-02-16  
20 <160> NUMBER OF SEQ ID NOS: 21  
22 <170> SOFTWARE: Microsoft Office 97  
24 <210> SEQ ID NO: 1  
25 <211> LENGTH: 2080  
26 <212> TYPE: DNA  
27 <213> ORGANISM: Dimorphotheca sinuata  
29 <400> SEQUENCE: 1  
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31 ttgaggacgc acccctactg aaccacaccg aaccaccacc accacccgcca ccccaactg 120  
32 ccggaagaaa acgggttggt atcaaggttg tgcgttat caccctactc attttgctta 180  
33 ttgttcagt ttgttctc aaccaacaaa attcaagtca ctccaccacc aattcaaaat 240  
34 ccatctccca atccgatcgc ctcatttggg aaagaacatc tttccatttt caacccgcca 300  
35 aaaatttcat ttacgatccc aatggggcat tatttcacat ggggtggtag catctttct 360  
36 atcaatacaa cccgtacggt cctgtttggg gaaataatgtc atggggtagtac tccgtttcca 420  
37 aagacatgat caactgggtt gagcttccag tcgcattggg cccaaaccgaa tggtagata 480  
38 tcgagggtgt tttatccggg tccaccaccg tcctcccaa cggtaaaatc ttgcattgt 540  
39 acacaggaaa cgctaacat ttctcccaaatacatgcaaa agctgtaccc gtcaacatata 600  
40 ctgaccact tcttacgcg tgggtcaaat acgatggtaa cccaaatccgt tataactccac 660  
41 cagggattgg gttaaaagac tatcgggacc cgtcaacagt ctggacgggt cccgatggaa 720  
42 aacatcgat gatcatggg tctaaacgaa acaaaaacggg actagtagtt gtttaccaca 780  
43 caaccgattt cacaattat gtgatgtcgg atgagccgtt gcattcggta cctaataccg 840  
44 atatgtggg atgcgttgac tttaccctgt ttcgttgac caatgatagc gcgcgttgata 900  
45 tggcggctt tgggtcggtt atcaaacacg tgattaaaga aagttggag ggacatggaa 960  
46 tggattggta ttgcattggg acttatgatg catcaaccga taaatggact cccgataacc 1020  
47 cgaaaatttata tgggtgtatc ggggtcgat gtgattacgg aagttttttt gcatcgaaga 1080  
48 gtctttcga tccgttgaag aaaaggaggg tgacttgggg ttatgttggg gaatcagata 1140  
49 aacctgatca ggaccttotct agaggatggg ctaccattta taatgttgcg cggacgggtgg 1200  
50 tactagatag aaagaccggaa acacatctac ttcatggcc agttgaagaa atcgagagtt 1260  
51 tgagatccaa tggtaagaa ttcaacggaa ttgaactcaa accgggttcg atcattccac 1320  
52 ttgacatagg ctcggctact cagttggaca tagttgcac atttgaagt gatcaagatg 1380  
53 cgttggaaaggc tataagtggaa accaacgaag aatataatttgc taccaaaagc tgggtgtcag 1440  
54 ccggaaagggg aagttgggaa ccatttgggg ttgcgtttt agccgatggaa acactttcag 1500  
55 agttaactcc cgtgtatttca tacatagcta aaaatacggta tggaaagtgtt gcaacacatt 1560  
56 tttgtaccga taagctaaaga tcatcaacttag attatgatcg tggaaagatgtt gtgtatggaa 1620  
57 gcactgtccc tggctgtatc ggtgaagaac tcacaatggat gttattgggtt gaccattcgg 1680  
58 tagtagaagg gtttgcgaa ggaggaaggaa cggtaataac atcaagggtt tatccgacaa 1740

ENTERED

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59 aggcaatata cgacaacgcg aagggtttct tattcaacaa cgctactgg acgagtgtga 1800  
60 aggctctct caagatggg caaatggctc ctgcccagat taaaccttac cctttttat 1860  
61 catatgtttc atttcaactt cactagaaca cttgtgtta ctattattgt atcttatatt 1920  
62 ttttatatgt acgtaataat taccgtttgg atgggtttgt tttgttcaac ctctgcattg 1980  
63 tgtgttaagt agtaagccgc gattattttt ataatatgaa taggttgttt tgttcaaaaa 2040  
64 aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa 2080  
66 <210> SEQ ID NO: 2  
67 <211> LENGTH: 608  
68 <212> TYPE: PRT  
69 <213> ORGANISM: Dimorphotheca sinuata  
71 <400> SEQUENCE: 2  
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73 1 5 10 15  
75 Asn His Thr Glu Pro Pro Pro Pro Pro Pro Pro Thr Ala Gly Arg  
76 20 25 30  
78 Lys Arg Leu Leu Ile Lys Val Val Ser Val Ile Thr Leu Leu Ile Leu  
79 35 40 45  
81 Leu Ile Val Ser Val Leu Phe Leu Asn Gln Gln Asn Ser Ser His Ser  
82 50 55 60  
84 Thr Thr Asn Ser Lys Ser Ile Ser Gln Ser Asp Arg Leu Ile Trp Glu  
85 65 70 75 80  
87 Arg Thr Ser Phe His Phe Gln Pro Ala Lys Asn Phe Ile Tyr Asp Pro  
88 85 90 95  
90 Asn Gly Pro Leu Phe His Met Gly Trp Tyr His Leu Phe Tyr Gln Tyr  
91 100 105 110  
93 Asn Pro Tyr Gly Pro Val Trp Gly Asn Met Ser Trp Gly His Ser Val  
94 115 120 125  
96 Ser Lys Asp Met Ile Asn Trp Phe Glu Leu Pro Val Ala Leu Val Pro  
97 130 135 140  
99 Thr Glu Trp Tyr Asp Ile Glu Gly Val Leu Ser Gly Ser Thr Thr Val  
100 145 150 155 160  
102 Leu Pro Asn Gly Gln Ile Phe Ala Leu Tyr Thr Gly Asn Ala Asn Asp  
103 165 170 175  
105 Phe Ser Gln Leu Gln Cys Lys Ala Val Pro Val Asn Ile Ser Asp Pro  
106 180 185 190  
108 Leu Leu Ile Glu Trp Val Lys Tyr Asp Gly Asn Pro Ile Leu Tyr Thr  
109 195 200 205  
111 Pro Pro Gly Ile Gly Leu Lys Asp Tyr Arg Asp Pro Ser Thr Val Trp  
112 210 215 220  
114 Thr Gly Pro Asp Gly Lys His Arg Met Ile Met Gly Ser Lys Arg Asn  
115 225 230 235 240  
117 Lys Thr Gly Leu Val Leu Val Tyr His Thr Thr Asp Phe Thr Asn Tyr  
118 245 250 255  
120 Val Met Ser Asp Glu Pro Leu His Ser Val Pro Asn Thr Asp Met Trp  
121 260 265 270  
123 Glu Cys Val Asp Phe Tyr Pro Val Ser Leu Thr Asn Asp Ser Ala Leu  
124 275 280 285  
126 Asp Met Ala Ala Tyr Gly Ser Gly Ile Lys His Val Ile Lys Glu Ser  
127 290 295 300

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Input Set : A:\BB1463 US NA Seq Listing.txt  
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129 Trp Glu Gly His Gly Met Asp Trp Tyr Ser Ile Gly Thr Tyr Asp Ala  
130 305 310 315 320  
132 Ser Thr Asp Lys Trp Thr Pro Asp Asn Pro Lys Leu Asp Val Gly Ile  
133 325 330 335  
135 Gly Leu Arg Cys Asp Tyr Gly Lys Phe Phe Ala Ser Lys Ser Leu Phe  
136 340 345 350  
138 Asp Pro Leu Lys Lys Arg Arg Val Thr Trp Gly Tyr Val Gly Glu Ser  
139 355 360 365  
141 Asp Lys Pro Asp Gln Asp Leu Ser Arg Gly Trp Ala Thr Ile Tyr Asn  
142 370 375 380  
144 Val Ala Arg Thr Val Val Leu Asp Arg Lys Thr Gly Thr His Leu Leu  
145 385 390 395 400  
147 His Trp Pro Val Glu Glu Ile Glu Ser Leu Arg Ser Asn Gly Gln Glu  
148 405 410 415  
150 Phe Asn Glu Ile Glu Leu Lys Pro Gly Ser Ile Ile Pro Leu Asp Ile  
151 420 425 430  
153 Gly Ser Ala Thr Gln Leu Asp Ile Val Ala Thr Phe Glu Val Asp Gln  
154 435 440 445  
156 Asp Ala Leu Lys Ala Ile Ser Glu Thr Asn Glu Glu Tyr Ile Cys Thr  
157 450 455 460  
159 Lys Ser Trp Gly Ala Ala Gly Arg Gly Ser Leu Gly Pro Phe Gly Val  
160 465 470 475 480  
162 Ala Val Leu Ala Asp Gly Thr Leu Ser Glu Leu Thr Pro Val Tyr Phe  
163 485 490 495  
165 Tyr Ile Ala Lys Asn Thr Asp Gly Ser Val Ala Thr His Phe Cys Thr  
166 500 505 510  
168 Asp Lys Leu Arg Ser Ser Leu Asp Tyr Asp Arg Glu Arg Val Val Tyr  
169 515 520 525  
171 Gly Ser Thr Val Pro Val Leu Asp Gly Glu Glu Leu Thr Met Arg Leu  
172 530 535 540  
174 Leu Val Asp His Ser Val Val Glu Gly Phe Ala Gln Gly Arg Thr  
175 545 550 555 560  
177 Val Ile Thr Ser Arg Val Tyr Pro Thr Lys Ala Ile Tyr Asp Asn Ala  
178 565 570 575  
180 Lys Val Phe Leu Phe Asn Asn Ala Thr Gly Thr Ser Val Lys Ala Ser  
181 580 585 590  
183 Leu Lys Ile Trp Gln Met Ala Pro Ala Gln Ile Lys Pro Tyr Pro Leu  
184 595 600 605  
186 <210> SEQ ID NO: 3  
187 <211> LENGTH: 2146  
188 <212> TYPE: DNA  
189 <213> ORGANISM: Parthenium argentatum Grey  
191 <400> SEQUENCE: 3  
192 gcacgaggag accagtcagc acacagtaac tgaactcaact caacccattta ttcacccatca 60  
193 ccatgacaac ccctgaacaa cccattacag accttgaaca cgaacccaaac cacaaccgca 120  
194 cacccttatt ggaccacaac gaatcacaac ccgtaaaagaa acatttggtc ttcaaaggatc 180  
195 tgtctgtgt tactttcatt tcattgttct ttatttctgc ttttttattc attgttttga 240  
196 accaacaatccat atatcggtta agtactcgca atccgatcgc cttacgtggg 300  
197 aacgaaccgc ttttcattttt caaccggcca agaattttat ttatgatccc aatggtaaaa 360

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198	tgtactacat	gggctggtag	catctattct	atcaatacaa	tccatacgca	ccggtttggg	420										
199	gtaatatgtc	atggggtcac	tccgtatcca	aagacatgtat	caactggtag	gagctacccg	480										
200	tcgctatagt	cccgactgaa	ttgttatgata	ttgagggcgt	cttatctggg	tccatcacag	540										
201	tgcttcccaa	cgggcagatc	tttgcattgt	acacggggaa	tgctaatgac	ttttcccaat	600										
202	tgcaatgcaa	agctgtaccc	gtgaactcat	ctgacccact	tcttgtttag	tgggtcaagt	660										
203	acgaagataa	cccaatcctg	tacactccac	cagggattgg	gttaaaagac	tatagggacc	720										
204	cgtcaacagt	ctggacgggt	cctgatggaa	agcataggat	gatcatggg	actaaacgtg	780										
205	gcaatacagg	aatgataactt	gtttaccata	ccactgatta	cacgaactat	gagatgttg	840										
206	atgagcctat	gcactcggtt	cccaataccg	atatgtgggaa	atgcgttgc	ttttacccgg	900										
207	tttcattaaac	caacgatagt	gcacttgata	ttgcggctca	cgggtcggt	atcaaacacg	960										
208	tgattaaaga	aagtggggag	ggatatgggaa	tggatttcta	ttcaatcggt	acttatgacg	1020										
209	catttaacga	taaatggact	cccgataacc	cagagttaga	tgttggtatac	gggttgcgg	1080										
210	gtgattacgg	tagttttt	gcatcaaaga	gtattttga	cccaagtgaag	aaaaggagga	1140										
211	tcacttgggc	ttatgttggaa	gaatcagata	atgctgtat	tgacctctcc	agaggatggg	1200										
212	ctactattta	taatgttggaa	agaactatgt	tactagatag	aaagaccggg	accattttac	1260										
213	ttcattggcc	tgtcgaggaa	atcgagatgt	tgagatacaa	tggtcaggaa	ttttaaagaga	1320										
214	tcaaaactaga	gcccgttca	attgctccac	tcgacatagg	caccgctaca	cagttggaca	1380										
215	tagttcaac	atthaagggt	gtgaggctg	cattgaacgc	gacaagtgaa	accgatgata	1440										
216	acttcgcttg	caccacgagc	tcaggtgcag	ttgaaagggg	aagtttgggaa	ccatttggc	1500										
217	ttgcggttct	agctgtatgg	accctttccg	agttaactcc	ggtttatattc	tacattgcta	1560										
218	aaaaggccga	tggaggtgt	tcaacacatt	tttgcaccga	taagctaagg	tcatccttgg	1620										
219	attttataaa	ggagagagatg	gtgtacggta	gcactgttcc	tgtgttagat	gatgaagaac	1680										
220	tcacaatgag	gctattggtg	gatcattcgg	tagtcagggc	gtttgcacaa	ggaggaagga	1740										
221	ttgccataac	atcaagggtg	tatccgacga	aagcaatata	cgaaggagcg	aagtgttct	1800										
222	tattcaacaa	tgccacggat	acgagtgtg	aggcatctct	caagatttgg	caaatggctt	1860										
223	ctgccccaaat	tcatcaatac	gagtttattt	agggctctc	gttatccctt	ttatttagtat	1920										
224	ttatgttattt	taattttattt	agacctatgt	atttgtat	atgatttctt	atcgtgctt	1980										
225	aagtagtaaa	tgaattgtgt	ttgggtaaaaa	aaataaaaaaa	aaaaaaaaaa	aaaaaaaaaa	2040										
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231	<211>	LENGTH:	609														
232	<212>	TYPE:	PRT														
233	<213>	ORGANISM:	Parthenium argentatum Grey														
235	<400>	SEQUENCE:	4														
236	Met	Thr	Thr	Pro	Glu	Gln	Pro	Ile	Thr	Asp	Leu	Glu	His	Glu	Pro	Asn	
237	1				5				10					15			
239	His	Asn	Arg	Thr	Pro	Leu	Leu	Asp	His	Asn	Glu	Ser	Gln	Pro	Val	Lys	
240						20				25				30			
242	Lys	His	Leu	Phe	Phe	Lys	Val	Leu	Ser	Gly	Val	Thr	Phe	Ile	Ser	Leu	
243						35			40			45					
245	Phe	Phe	Ile	Ser	Ala	Phe	Leu	Phe	Ile	Val	Leu	Asn	Gln	Gln	Asn	Ser	
246						50			55			60					
248	Thr	Asn	Ile	Ser	Val	Lys	Tyr	Ser	Gln	Ser	Asp	Arg	Leu	Thr	Trp	Glu	
249						65			70			75			80		
251	Arg	Thr	Ala	Phe	His	Phe	Gln	Pro	Ala	Lys	Asn	Phe	Ile	Tyr	Asp	Pro	
252									85			90			95		
254	Asn	Gly	Gln	Met	Tyr	Tyr	Met	Gly	Trp	Tyr	His	Leu	Phe	Tyr	Gln	Tyr	
255									100			105			110		

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257 Asn Pro Tyr Ala Pro Val Trp Gly Asn Met Ser Trp Gly His Ser Val  
258 115 120 125  
260 Ser Lys Asp Met Ile Asn Trp Tyr Glu Leu Pro Val Ala Ile Val Pro  
261 130 135 140  
263 Thr Glu Trp Tyr Asp Ile Glu Gly Val Leu Ser Gly Ser Ile Thr Val  
264 145 150 155 160  
266 Leu Pro Asn Gly Gln Ile Phe Ala Leu Tyr Thr Gly Asn Ala Asn Asp  
267 165 170 175  
269 Phe Ser Gln Leu Gln Cys Lys Ala Val Pro Val Asn Ser Ser Asp Pro  
270 180 185 190  
272 Leu Leu Val Glu Trp Val Lys Tyr Glu Asp Asn Pro Ile Leu Tyr Thr  
273 195 200 205  
275 Pro Pro Gly Ile Gly Leu Lys Asp Tyr Arg Asp Pro Ser Thr Val Trp  
276 210 215 220  
278 Thr Gly Pro Asp Gly Lys His Arg Met Ile Met Gly Thr Lys Arg Gly  
279 225 230 235 240  
281 Asn Thr Gly Met Ile Leu Val Tyr His Thr Thr Asp Tyr Thr Asn Tyr  
282 245 250 255  
284 Glu Met Leu Asn Glu Pro Met His Ser Val Pro Asn Thr Asp Met Trp  
285 260 265 270  
287 Glu Cys Val Asp Phe Tyr Pro Val Ser Leu Thr Asn Asp Ser Ala Leu  
288 275 280 285  
290 Asp Ile Ala Ala Tyr Gly Ser Gly Ile Lys His Val Ile Lys Glu Ser  
291 290 295 300  
293 Trp Glu Gly Tyr Gly Met Asp Phe Tyr Ser Ile Gly Thr Tyr Asp Ala  
294 305 310 315 320  
296 Phe Asn Asp Lys Trp Thr Pro Asp Asn Pro Glu Leu Asp Val Gly Ile  
297 325 330 335  
299 Gly Leu Arg Cys Asp Tyr Gly Arg Phe Phe Ala Ser Lys Ser Ile Phe  
300 340 345 350  
302 Asp Pro Val Lys Lys Arg Arg Ile Thr Trp Ala Tyr Val Gly Glu Ser  
303 355 360 365  
305 Asp Asn Ala Asp Asp Asp Leu Ser Arg Gly Trp Ala Thr Ile Tyr Asn  
306 370 375 380  
308 Val Gly Arg Thr Ile Val Leu Asp Arg Lys Thr Gly Thr His Leu Leu  
309 385 390 395 400  
311 His Trp Pro Val Glu Glu Ile Glu Ser Leu Arg Tyr Asn Gly Gln Glu  
312 405 410 415  
314 Phe Lys Glu Ile Lys Leu Glu Pro Gly Ser Ile Ala Pro Leu Asp Ile  
315 420 425 430  
317 Gly Thr Ala Thr Gln Leu Asp Ile Val Ala Thr Phe Lys Val Asp Glu  
318 435 440 445  
320 Ala Ala Leu Asn Ala Thr Ser Glu Thr Asp Asp Asn Phe Ala Cys Thr  
321 450 455 460  
323 Thr Ser Ser Gly Ala Val Glu Arg Gly Ser Leu Gly Pro Phe Gly Leu  
324 465 470 475 480  
326 Ala Val Leu Ala Asp Gly Thr Leu Ser Glu Leu Thr Pro Val Tyr Phe  
327 485 490 495  
329 Tyr Ile Ala Lys Lys Ala Asp Gly Gly Val Ser Thr His Phe Cys Thr

VERIFICATION SUMMARY  
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L:11 M:270 C: Current Application Number differs, Replaced Application Number  
L:12 M:271 C: Current Filing Date differs, Replaced Current Filing Date